

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/532,683
Source: IFP
Date Processed by STIC: 8/2/06

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IFWP

RAW SEQUENCE LISTING

DATE: 08/02/2006

PATENT APPLICATION: US/10/532,683

TIME: 08:46:46

Input Set : A:\2005_0716A Sequence.txt

Output Set: N:\CRF4\08022006\J532683.raw

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3 <110> APPLICANT: Ishihara Sangyo Kaisha, Ltd.
5 <120> TITLE OF INVENTION: Regulation of RAPL-Rap1 Interaction
7 <130> FILE REFERENCE: IS-08PCT
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/532,683
C--> 9 <141> CURRENT FILING DATE: 2005-04-26
9 <150> PRIOR APPLICATION NUMBER: JP 2002-316892
10 <151> PRIOR FILING DATE: 2002-10-30
12 <160> NUMBER OF SEQ ID NOS: 14
14 <170> SOFTWARE: PatentIn version 3.1
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 555
18 <212> TYPE: DNA
19 <213> ORGANISM: Homo sapiens
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (1)..(555)
24 <223> OTHER INFORMATION: Human Rap1
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29 Met Arg Glu Tyr Lys Leu Val Val Leu Gly Ser Gly Gly Val Gly Lys
30 1          5          10          15
32 tct gct ctg aca gtt cag ttt gtt cag gga att ttt gtt gaa aaa tat      96
33 Ser Ala Leu Thr Val Gln Phe Val Gln Gly Ile Phe Val Glu Lys Tyr
34          20          25          30
36 gac cca acg ata gaa gat tcc tac aga aag caa gtt gaa gtc gat tgc      144
37 Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Glu Val Asp Cys
38          35          40          45
40 caa cag tgt atg ctc gaa atc ctg gat act gca ggg aca gag caa ttt      192
41 Gln Gln Cys Met Leu Glu Ile Leu Asp Thr Ala Gly Thr Glu Gln Phe
42          50          55          60
44 aca gca atg agg gat ttg tat atg aag aac ggc caa ggt ttt gca cta      240
45 Thr Ala Met Arg Asp Leu Tyr Met Lys Asn Gly Gln Gly Phe Ala Leu
46 65          70          75          80
48 gta tat tct att aca gct cag tcc acg ttt aac gac tta cag gac ctg      288
49 Val Tyr Ser Ile Thr Ala Gln Ser Thr Phe Asn Asp Leu Gln Asp Leu
50          85          90          95
52 agg gaa cag att tta cgg gtt aag gac acg gaa gat gtt cca atg att      336
53 Arg Glu Gln Ile Leu Arg Val Lys Asp Thr Glu Asp Val Pro Met Ile
54          100          105          110
56 ttg gtt ggc aat aaa tgt gac ctg gaa gat gag cga gta gtt ggc aaa      384
57 Leu Val Gly Asn Lys Cys Asp Leu Glu Asp Glu Arg Val Val Gly Lys
58          115          120          125
60 gag cag ggc cag aat tta gca aga cag tgg tgt aac tgt gcc ttt tta      432

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61 Glu Gln Gly Gln Asn Leu Ala Arg Gln Trp Cys Asn Cys Ala Phe Leu
62      130                      135                      140
64 gaa tct tct gca aag tca aag atc aat gtt aat gag ata ttt tat gac      480
65 Glu Ser Ser Ala Lys Ser Lys Ile Asn Val Asn Glu Ile Phe Tyr Asp
66 145                      150                      155                      160
68 ctg gtc aga cag ata aat agg aaa aca cca gtg gaa aag aag aag cct      528
69 Leu Val Arg Gln Ile Asn Arg Lys Thr Pro Val Glu Lys Lys Lys Pro
70                      165                      170                      175
72 aaa aag aaa tca tgt ctg ctg ctc tag      555
73 Lys Lys Lys Ser Cys Leu Leu Leu
74      180
77 <210> SEQ ID NO: 2
78 <211> LENGTH: 184
79 <212> TYPE: PRT
80 <213> ORGANISM: Homo sapiens
82 <400> SEQUENCE: 2
84 Met Arg Glu Tyr Lys Leu Val Val Leu Gly Ser Gly Gly Val Gly Lys
85 1                      5                      10                      15
88 Ser Ala Leu Thr Val Gln Phe Val Gln Gly Ile Phe Val Glu Lys Tyr
89      20                      25                      30
92 Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Glu Val Asp Cys
93      35                      40                      45
96 Gln Gln Cys Met Leu Glu Ile Leu Asp Thr Ala Gly Thr Glu Gln Phe
97      50                      55                      60
100 Thr Ala Met Arg Asp Leu Tyr Met Lys Asn Gly Gln Gly Phe Ala Leu
101 65                      70                      75                      80
104 Val Tyr Ser Ile Thr Ala Gln Ser Thr Phe Asn Asp Leu Gln Asp Leu
105      85                      90                      95
108 Arg Glu Gln Ile Leu Arg Val Lys Asp Thr Glu Asp Val Pro Met Ile
109      100                     105                     110
112 Leu Val Gly Asn Lys Cys Asp Leu Glu Asp Glu Arg Val Val Gly Lys
113      115                     120                     125
116 Glu Gln Gly Gln Asn Leu Ala Arg Gln Trp Cys Asn Cys Ala Phe Leu
117      130                     135                     140
120 Glu Ser Ser Ala Lys Ser Lys Ile Asn Val Asn Glu Ile Phe Tyr Asp
121 145                     150                     155                     160
124 Leu Val Arg Gln Ile Asn Arg Lys Thr Pro Val Glu Lys Lys Lys Pro
125      165                     170                     175
128 Lys Lys Lys Ser Cys Leu Leu Leu
129      180
132 <210> SEQ ID NO: 3
133 <211> LENGTH: 798
134 <212> TYPE: DNA
135 <213> ORGANISM: Homo sapiens
137 <220> FEATURE:
138 <221> NAME/KEY: CDS
139 <222> LOCATION: (1)..(798)
140 <223> OTHER INFORMATION: Human RAPL (or Human p30)
143 <400> SEQUENCE: 3

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144	atg acc gtg gac agc agc atg agc agt ggg tac tgc agc ctg gac gag	48
145	Met Thr Val Asp Ser Ser Met Ser Ser Gly Tyr Cys Ser Leu Asp Glu	
146	1 5 10 15	
148	gaa ctg gaa gac tgc ttc ttc act gct aag act acc ttt ttc aga aat	96
149	Glu Leu Glu Asp Cys Phe Phe Thr Ala Lys Thr Thr Phe Phe Arg Asn	
150	20 25 30	
152	gcg cag agc aaa cat ctt tca aag aat gtc tgt aaa cct gtg gag gaa	144
153	Ala Gln Ser Lys His Leu Ser Lys Asn Val Cys Lys Pro Val Glu Glu	
154	35 40 45	
156	aca cag cgc ccg ccc aca ctg cag gag atc aag cag aag atc gac agc	192
157	Thr Gln Arg Pro Pro Thr Leu Gln Glu Ile Lys Gln Lys Ile Asp Ser	
158	50 55 60	
160	tac aac acg cga gag aag aac tgc ctg ggc atg aaa ctg agt gaa gac	240
161	Tyr Asn Thr Arg Glu Lys Asn Cys Leu Gly Met Lys Leu Ser Glu Asp	
162	65 70 75 80	
164	ggc acc tac acg ggt ttc atc aaa gtg cat ctg aaa ctc cgg cgg cct	288
165	Gly Thr Tyr Thr Gly Phe Ile Lys Val His Leu Lys Leu Arg Arg Pro	
166	85 90 95	
168	gtg acg gtg cct gct ggg atc cgg ccc cag tcc atc tat gat gcc atc	336
169	Val Thr Val Pro Ala Gly Ile Arg Pro Gln Ser Ile Tyr Asp Ala Ile	
170	100 105 110	
172	aag gag gtg aac ctg gcg gct acc acg gac aag cgg aca tcc ttc tac	384
173	Lys Glu Val Asn Leu Ala Ala Thr Thr Asp Lys Arg Thr Ser Phe Tyr	
174	115 120 125	
176	ctg ccc cta gat gcc atc aag cag ctg cac atc agc agc acc acc acc	432
177	Leu Pro Leu Asp Ala Ile Lys Gln Leu His Ile Ser Ser Thr Thr Thr	
178	130 135 140	
180	gtc agt gag gtc atc cag ggg ctg ctc aag aag ttc atg gtt gtg gac	480
181	Val Ser Glu Val Ile Gln Gly Leu Leu Lys Lys Phe Met Val Val Asp	
182	145 150 155 160	
184	aat ccc cag aag ttt gca ctt ttt aag cgg ata cac aag gac gga caa	528
185	Asn Pro Gln Lys Phe Ala Leu Phe Lys Arg Ile His Lys Asp Gly Gln	
186	165 170 175	
188	gtg ctc ttc cag aaa ctc tcc att gct gac cgc ccc ctc tac ctg cgc	576
189	Val Leu Phe Gln Lys Leu Ser Ile Ala Asp Arg Pro Leu Tyr Leu Arg	
190	180 185 190	
192	ctg ctt gct ggg cct gac acg gag gtc ctc agc ttt gtg cta aag gag	624
193	Leu Leu Ala Gly Pro Asp Thr Glu Val Leu Ser Phe Val Leu Lys Glu	
194	195 200 205	
196	aat gaa act gga gag gta gag tgg gat gcc ttc tcc atc cct gaa ctt	672
197	Asn Glu Thr Gly Glu Val Glu Trp Asp Ala Phe Ser Ile Pro Glu Leu	
198	210 215 220	
200	cag aac ttc cta aca atc ctg gaa aaa gag gag cag gac aaa atc caa	720
201	Gln Asn Phe Leu Thr Ile Leu Glu Lys Glu Glu Gln Asp Lys Ile Gln	
202	225 230 235 240	
204	caa gtg caa aag aag tat gac aag ttt agg cag aaa ctg gag gag gcc	768
205	Gln Val Gln Lys Lys Tyr Asp Lys Phe Arg Gln Lys Leu Glu Glu Ala	
206	245 250 255	
208	tta aga gaa tcc cag ggc aaa cct ggg taa	798

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209 Leu Arg Glu Ser Gln Gly Lys Pro Gly
210                260                265
213 <210> SEQ ID NO: 4
214 <211> LENGTH: 265
215 <212> TYPE: PRT
216 <213> ORGANISM: Homo sapiens
218 <400> SEQUENCE: 4
220 Met Thr Val Asp Ser Ser Met Ser Ser Gly Tyr Cys Ser Leu Asp Glu
221 1                5                10                15
224 Glu Leu Glu Asp Cys Phe Phe Thr Ala Lys Thr Thr Phe Phe Arg Asn
225                20                25                30
228 Ala Gln Ser Lys His Leu Ser Lys Asn Val Cys Lys Pro Val Glu Glu
229                35                40                45
232 Thr Gln Arg Pro Pro Thr Leu Gln Glu Ile Lys Gln Lys Ile Asp Ser
233                50                55                60
236 Tyr Asn Thr Arg Glu Lys Asn Cys Leu Gly Met Lys Leu Ser Glu Asp
237 65                70                75                80
240 Gly Thr Tyr Thr Gly Phe Ile Lys Val His Leu Lys Leu Arg Arg Pro
241                85                90                95
244 Val Thr Val Pro Ala Gly Ile Arg Pro Gln Ser Ile Tyr Asp Ala Ile
245                100               105               110
248 Lys Glu Val Asn Leu Ala Ala Thr Thr Asp Lys Arg Thr Ser Phe Tyr
249                115               120               125
252 Leu Pro Leu Asp Ala Ile Lys Gln Leu His Ile Ser Ser Thr Thr Thr
253                130               135               140
256 Val Ser Glu Val Ile Gln Gly Leu Leu Lys Lys Phe Met Val Val Asp
257 145               150               155               160
260 Asn Pro Gln Lys Phe Ala Leu Phe Lys Arg Ile His Lys Asp Gly Gln
261                165               170               175
264 Val Leu Phe Gln Lys Leu Ser Ile Ala Asp Arg Pro Leu Tyr Leu Arg
265                180               185               190
268 Leu Leu Ala Gly Pro Asp Thr Glu Val Leu Ser Phe Val Leu Lys Glu
269                195               200               205
272 Asn Glu Thr Gly Glu Val Glu Trp Asp Ala Phe Ser Ile Pro Glu Leu
273                210               215               220
276 Gln Asn Phe Leu Thr Ile Leu Glu Lys Glu Glu Gln Asp Lys Ile Gln
277 225               230               235               240
280 Gln Val Gln Lys Lys Tyr Asp Lys Phe Arg Gln Lys Leu Glu Glu Ala
281                245               250               255
284 Leu Arg Glu Ser Gln Gly Lys Pro Gly
285                260                265
288 <210> SEQ ID NO: 5
289 <211> LENGTH: 498
290 <212> TYPE: DNA
291 <213> ORGANISM: Homo sapiens
293 <220> FEATURE:
294 <221> NAME/KEY: CDS
295 <222> LOCATION: (1)..(498)
296 <223> OTHER INFORMATION: Dominant-Negative Human RAPL

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299 <400> SEQUENCE: 5
300 gct ggg atc cgg ccc cag tcc atc tat gat gcc atc aag gag gtg aac      48
301 Ala Gly Ile Arg Pro Gln Ser Ile Tyr Asp Ala Ile Lys Glu Val Asn
302 1          5          10          15
304 ctg gcg gct acc acg gac aag cgg aca tcc ttc tac ctg ccc cta gat      96
305 Leu Ala Ala Thr Thr Asp Lys Arg Thr Ser Phe Tyr Leu Pro Leu Asp
306          20          25          30
308 gcc atc aag cag ctg cac atc agc agc acc acc acc gtc agt gag gtc      144
309 Ala Ile Lys Gln Leu His Ile Ser Ser Thr Thr Thr Val Ser Glu Val
310          35          40          45
312 atc cag ggg ctg ctc aag aag ttc atg gtt gtg gac aat ccc cag aag      192
313 Ile Gln Gly Leu Leu Lys Lys Phe Met Val Val Asp Asn Pro Gln Lys
314          50          55          60
316 ttt gca ctt ttt aag cgg ata cac aag gac gga caa gtg ctc ttc cag      240
317 Phe Ala Leu Phe Lys Arg Ile His Lys Asp Gly Gln Val Leu Phe Gln
318 65          70          75          80
320 aaa ctc tcc att gct gac cgc ccc ctc tac ctg cgc ctg ctt gct ggg      288
321 Lys Leu Ser Ile Ala Asp Arg Pro Leu Tyr Leu Arg Leu Leu Ala Gly
322          85          90          95
324 cct gac acg gag gtc ctc agc ttt gtg cta aag gag aat gaa act gga      336
325 Pro Asp Thr Glu Val Leu Ser Phe Val Leu Lys Glu Asn Glu Thr Gly
326          100          105          110
328 gag gta gag tgg gat gcc ttc tcc atc cct gaa ctt cag aac ttc cta      384
329 Glu Val Glu Trp Asp Ala Phe Ser Ile Pro Glu Leu Gln Asn Phe Leu
330          115          120          125
332 aca atc ctg gaa aaa gag gag cag gac aaa atc caa caa gtg caa aag      432
333 Thr Ile Leu Glu Lys Glu Glu Gln Asp Lys Ile Gln Gln Val Gln Lys
334          130          135          140
336 aag tat gac aag ttt agg cag aaa ctg gag gag gcc tta aga gaa tcc      480
337 Lys Tyr Asp Lys Phe Arg Gln Lys Leu Glu Glu Ala Leu Arg Glu Ser
338 145          150          155          160
340 cag ggc aaa cct ggg taa      498
341 Gln Gly Lys Pro Gly
342          165
345 <210> SEQ ID NO: 6
346 <211> LENGTH: 165
347 <212> TYPE: PRT
348 <213> ORGANISM: Homo sapiens
350 <400> SEQUENCE: 6
352 Ala Gly Ile Arg Pro Gln Ser Ile Tyr Asp Ala Ile Lys Glu Val Asn
353 1          5          10          15
356 Leu Ala Ala Thr Thr Asp Lys Arg Thr Ser Phe Tyr Leu Pro Leu Asp
357          20          25          30
360 Ala Ile Lys Gln Leu His Ile Ser Ser Thr Thr Thr Val Ser Glu Val
361          35          40          45
364 Ile Gln Gly Leu Leu Lys Lys Phe Met Val Val Asp Asn Pro Gln Lys
365          50          55          60
368 Phe Ala Leu Phe Lys Arg Ile His Lys Asp Gly Gln Val Leu Phe Gln
369 65          70          75          80

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/532,683

DATE: 08/02/2006

TIME: 08:46:47

Input Set : A:\2005_0716A Sequence.txt

Output Set: N:\CRF4\08022006\J532683.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date